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imputing a plurality of probe intensities for a plurality of nucleic acid probes, each probe intensity indicating an extent of hybridization of a nucleic acid probe with at least one nucleic acid sequence including said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

said computer system comparing said plurality of probe intensities to each other; and

said computer system generating a base call identifying said unknown base according to results of said comparing step.

61. The method of claim 60, wherein said comparing step includes the step of said computer system calculating a ratio of a higher probe intensity to a lower probe intensity.

62. (Amended) The method of claim 61, wherein said generating [~~identifying~~] step includes the step of identifying said unknown base according to a nucleic acid probe having said higher probe intensity if said ratio is greater than a predetermined ratio value.

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63. The method of claim 62, wherein said predetermined ratio value is approximately 1.2.

64. (Amended) ~~The~~ method of claim 60, further comprising the step of sorting said plurality of probe intensities by intensity before said comparing step.

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65. The method of claim 60, wherein said at least one sequence includes a reference sequence.

66. The method of claim 65, wherein said comparing step includes the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to said probe hybridizing with said reference sequence.

67. The method of claim 65, wherein said comparing step includes the step of calculating first ratios of a wild-type probe intensity to each probe intensity of probes hybridizing with said reference sequence, wherein

said wild-type probe intensity indicates an extent of hybridization of a complementary probe with said reference sequence.

68. The method of claim 67, wherein said comparing step includes the step of calculating second ratios of the highest probe intensity of a probe hybridizing with said sample sequence to each probe intensity of probes hybridizing with said sample sequence.

69. The method of claim 68, wherein said comparing step includes the step of calculating third ratios of said first ratios to said second ratios.

①4 70. (Amended) The method of claim 69, wherein said generating [~~identifying~~] step includes the step of identifying said unknown base according to a base of said probe associated with a highest third ratio.

71. The method of claim 68, wherein said comparing step includes the step of calculating a ratio of a highest probe intensity of a probe hybridizing with said reference sequence to a highest intensity of a probe hybridizing with said sample sequence.

72. --CANCELED--

73. The method of claim 65, wherein probe intensities of probes hybridizing with said reference sequence are from a plurality of experiments.

74. The method of claim 73, wherein said comparing step includes the step of said computer system comparing probe intensities of probes hybridizing with said sample sequence to statistics about said plurality of experiments.

75. The method of claim 74, wherein said statistics include a mean and standard deviation.

76. The method of claim 73, further comprising the step of normalizing said plurality of probe intensities by dividing each probe intensity by a sum of related probe intensities, wherein related probe intensities are from probes that differ by a single base.

77. The method of claim 60, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

78. The method of claim 60, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

79. The method of claim 60, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

80. The method of claim 60, wherein said unknown base is identified as being A, C, G, or T.

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81. (Amended) In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:
imputing a plurality of probe intensities for a plurality of nucleic acid probes, each probe intensity indicating an extent of hybridization of a nucleic acid probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base;
said computer system calculating a ratio of a higher probe intensity to a lower probe intensity; and
said computer system generating a base call identifying said unknown base according to a base of a nucleic acid probe having said higher probe intensity if said ratio is greater than a predetermined ratio value.

82. The method of claim 81, wherein said predetermined ratio value is approximately 1.2.

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83. (Amended) The method of claim 81, further comprising the step of sorting said plurality of probe intensities by intensity before said comparing step.

84. The method of claim 81, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

85. The method of claim 81, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

86. The method of claim 81, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

87. The method of claim 81, wherein said unknown base is identified as being A, C, G, or T.

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88. (Amended) In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:
imputing a first set of probe intensities, each probe intensity in said first set indicating an extent of hybridization of a nucleic acid probe with a reference nucleic acid sequence, and each nucleic acid probe differing from each other by at least a single base;

imputing a second set of probe intensities, each probe intensity in said second set indicating an extent of hybridization of a nucleic acid probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

said computer system comparing at least one of said probe intensities in said first set and at least one of said probe intensities in said second set; and
said computer system generating a base call identifying said unknown base according to results of said comparing step.

89. The method of claim 88, wherein said comparing step includes the step of calculating first ratios of a wild-type probe intensity to each probe intensity of probes hybridizing with said reference sequence, wherein said wild-type probe intensity indicates an extent of hybridization of a complementary probe with said reference sequence.

90. The method of claim 89, wherein said comparing step includes the step of calculating second ratios of the highest probe intensity of probes hybridizing with said sample sequence to each probe intensity of a probe hybridizing with said sample sequence.

91. The method of claim 90, wherein said comparing step further includes the step of calculating third ratios of said first ratios to said second ratios.

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92. (Amended) The method of claim 91, wherein said ~~generating~~ [identifying] step includes the step of identifying said unknown base according to a base of said probe associated with a highest third ratio.

93. The method of claim 88, wherein said comparing step includes the step of calculating a ratio of a highest probe intensity in said first set to a highest intensity in said second set.

94. --CANCELED-- 6

95. The method of claim 88, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

96. The method of claim 88, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

97. The method of claim 88, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

98. The method of claim 88, wherein said unknown base is identified as being A, C, G, or T.

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99. (Amended) In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

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imputing statistics about a plurality of experiments, each of said experiments producing probe intensities, each probe intensity indicating an extent of hybridization of a nucleic acid probe with a reference nucleic acid sequence, and each nucleic acid probe differing from each other by at least a single base; imputing a plurality of probe intensities, each probe intensity indicating an extent of hybridization of a nucleic acid

probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base; said computer system comparing at least one of said plurality of probe intensities with said statistics; and said computer system generating a base call identifying said unknown base according to results of said comparing step.

100. The method of claim 99, wherein said statistics include a mean and standard deviation.

101. The method of claim 99, further comprising the step of normalizing said plurality of probe intensities by dividing each probe intensity by a sum of related probe intensities, wherein related probe intensities are from probes that differ by a single base.

102. The method of claim 99, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

103. The method of claim 99, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

104. The method of claim 99, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

105. The method of claim 99, wherein said unknown base is identified as being A, C, G, or T.

Please add new claims 106-117 as follows.

106. The method of claim 60, wherein the plurality of nucleic acid probes are in an array of probes.

107. The method of claim 60, wherein the plurality of probe intensities are fluorescent intensities.

108. A computer program product that identifies an unknown base in a sample nucleic acid sequence, comprising:

3 computer code that receives a plurality of probe
4 intensities for a plurality of nucleic acid probes, each probe
5 intensity indicating an extent of hybridization of a nucleic acid
6 probe with at least one nucleic acid sequence including said
7 sample sequence, and each nucleic acid probe differing from each
8 other by at least a single base;
9 computer code that performs a comparison of said
10 plurality of probe intensities to each other;
11 computer code that generates a base call identifying
12 said unknown base according to results of said comparison; and
13 a computer readable medium that stores said computer
14 codes.

109. A computer program product that identifies an
2 unknown base in a sample nucleic acid sequence, comprising:
3 computer code that receives a plurality of probe
4 intensities for a plurality of nucleic acid probes, each probe
5 intensity indicating an extent of hybridization of a nucleic acid
6 probe with said sample sequence, and each nucleic acid probe
7 differing from each other by at least a single base;
8 computer code that calculates a ratio of a higher probe
9 intensity to a lower probe intensity;
10 computer code that generates a base call identifying
11 said unknown base according to a base of a nucleic acid probe
12 having said higher probe intensity if said ratio is greater than
13 a predetermined ratio value; and
14 a computer readable medium that stores said computer
15 codes.

110. A computer program product that identifies an
2 unknown base in a sample nucleic acid sequence, comprising:
3 computer code that receives a first set of probe
4 intensities, each probe intensity in said first set indicating an
5 extent of hybridization of a nucleic acid probe with a reference
6 nucleic acid sequence, and each nucleic acid probe differing from
7 each other by at least a single base;

computer code that receives a second set of probe intensities, each probe intensity in said second set indicating an extent of hybridization of a nucleic acid probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

computer code that performs a comparison of at least one of said probe intensities in said first set and at least one of said probe intensities in said second set;

computer code that generates a base call identifying said unknown base according to results of said comparison; and
a computer readable medium that stores said computer codes.

111. A computer program product that identifies an unknown base in a sample nucleic acid sequence, comprising:
computer code that receives statistics about a plurality of experiments, each of said experiments producing probe intensities, each probe intensity indicating an extent of hybridization of a nucleic acid probe with a reference nucleic acid sequence, and each nucleic acid probe differing from each other by at least a single base;

computer code that receives a plurality of probe intensities, each probe intensity indicating an extent of hybridization of a nucleic acid probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

computer code that performs a comparison of at least one of said plurality of probe intensities with said statistics;

computer code that generates a base call identifying said unknown base according to results of said comparison; and
a computer readable medium that stores said computer codes.

112. A system that identifies an unknown base in a sample nucleic acid sequence, comprising:
a processor; and

4 a computer readable medium coupled to said processor
5 for storing a computer program comprising:
6 computer code that receives a plurality of probe
7 intensities for a plurality of nucleic acid probes, each probe
8 intensity indicating an extent of hybridization of a nucleic acid
9 probe with at least one nucleic acid sequence including said
10 sample sequence, and each nucleic acid probe differing from each
11 other by at least a single base;
12 computer code that performs a comparison of said
13 plurality of probe intensities to each other; and
14 computer code that generates a base call identifying
15 said unknown base according to results of said comparison.

113. A system that identifies an unknown base in a
sample nucleic acid sequence, comprising:
a processor; and
a computer readable medium coupled to said processor
for storing a computer program comprising:
computer code that receives a plurality of probe
intensities for a plurality of nucleic acid probes, each probe
intensity indicating an extent of hybridization of a nucleic acid
probe with said sample sequence, and each nucleic acid probe
differing from each other by at least a single base;
computer code that calculates a ratio of a higher probe
intensity to a lower probe intensity; and
computer code that generates a base call identifying
said unknown base according to a base of a nucleic acid probe
having said higher probe intensity if said ratio is greater than
a predetermined ratio value.

114. A system that identifies an unknown base in a
sample nucleic acid sequence, comprising:
a processor; and
a computer readable medium coupled to said processor
for storing a computer program comprising:
computer code that receives a first set of probe
intensities, each probe intensity in said first set indicating an

8 extent of hybridization of a nucleic acid probe with a reference
9 nucleic acid sequence, and each nucleic acid probe differing from
10 each other by at least a single base;

11 computer code that receives a second set of probe
12 intensities, each probe intensity in said second set indicating
13 an extent of hybridization of a nucleic acid probe with said
14 sample sequence, and each nucleic acid probe differing from each
15 other by at least a single base;

16 computer code that performs a comparison of at least
17 one of said probe intensities in said first set and at least one
18 of said probe intensities in said second set; and

19 computer code that generates a base call identifying
20 said unknown base according to results of said comparison.

1 115. A system that identifies an unknown base in a
2 sample nucleic acid sequence, comprising:

3 a processor; and

4 a computer readable medium coupled to said processor
5 for storing a computer program comprising:

6 computer code that receives statistics about a
7 plurality of experiments, each of said experiments producing
8 probe intensities, each probe intensity indicating an extent of
9 hybridization of a nucleic acid probe with a reference nucleic
10 acid sequence, and each nucleic acid probe differing from each
11 other by at least a single base;

12 computer code that receives a plurality of probe
13 intensities, each probe intensity indicating an extent of
14 hybridization of a nucleic acid probe with said sample sequence,
15 and each nucleic acid probe differing from each other by at least
16 a single base;

17 computer code that performs a comparison of at least
18 one of said plurality of probe intensities with said statistics;
19 and

20 computer code that generates a base call identifying
21 said unknown base according to results of said comparison.--

1 116. A system according to claims 112, 113, 114, or
2 115, wherein the plurality of nucleic acid probes are in an array
3 of probes.

1 117. A system according to claims 112, 113, 114, or
2 115, wherein the plurality of probe intensities are fluorescent
3 intensities.--

REMARKS

Claims 60-71, 73-93, and 95-117 are pending in the subject application. Applicants canceled claims 72 and 94 without prejudice and reserve all right to pursue these or other claims in another application. Claims 106-117 were added by this Amendment. In light of the amendments and following remarks, Applicants believe all claims now pending are in condition for allowance.

The Examiner indicated that claims 60-105 were allowable over the cited art, however, the disclosure was objected to because the Sequence Listing did not conform to 37 C.F.R. §§ 1.821-25. Additionally, claims 60-105 were rejected under 35 U.S.C. § 101 as being directed at non-statutory subject matter and under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject invention.

The Sequence Listing

The Office Action mailed July 9, 1996 did not include a Notice to Comply. Applicants telephoned the Examiner on July 17, 1996 to inform her that the Notice had not been received. Applicants appreciate the Examiner's diligence in faxing the Sequence Verification Report (enclosed) to the undersigned's attention on August 22, 1996.

Applicants corrected the Sequence Listing to remedy errors specified in the faxed Report. The corrections include replacing each occurrence of 'X' in the Sequence Listing with an 'N' (both were utilized in the specification to indicate an